

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 12, 2005, 19:28:11 ; Search time 161 Seconds  
(without alignments)  
48.998 Million cell updates/sec

Title: US-09-777-560-1

Perfect score: 90  
Sequence: 1 RRKKAVALLPVALLALAP 20

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1777461 seqs, 394431504 residues

Total number of hits satisfying chosen parameters: 1777461

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
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15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep:\*  
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18: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
19: /cgn2\_6/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*  
20: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*  
21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	90	100.0	20	12	US-09-777-560-1
2	90	100.0	20	12	US-09-777-560-2
3	80	88.9	29	15	US-10-126-103-124
4	80	88.9	29	15	US-10-431-096-124
5	80	88.9	29	17	US-10-858-367-60
6	75	83.3	17	12	US-09-777-560-27
7	72.5	80.6	20	12	US-09-777-560-3
8	70	77.8	16	9	US-09-214-371-45
9	70	77.8	16	9	US-09-811-870-5
10	70	77.8	16	9	US-09-785-802A-9
11	70	77.8	16	10	US-09-962-967A-3

12	70	77.8	16	10	US-09-965-876A-3	Sequence 3, Appl1
13	70	77.8	16	10	US-09-789-831-12	Sequence 12, Appl1
14	70	77.8	16	14	US-10-226-956-285	Sequence 285, App
15	70	77.8	16	14	US-10-077-555-7	Sequence 7, Appl1
16	70	77.8	16	14	US-10-211-088-103	Sequence 303, App
17	70	77.8	16	14	US-10-136-728-18	Sequence 18, Appl1
18	70	77.8	16	14	US-10-156-570A-26	Sequence 26, Appl1
19	70	77.8	16	15	US-10-144-559-18	Sequence 18, Appl1
20	70	77.8	16	15	US-10-185-593-4	Sequence 4, Appl1
21	70	77.8	16	15	US-10-233-410-1	Sequence 22, Appl1
22	70	77.8	16	15	US-10-261-161-22	Sequence 27, Appl1
23	70	77.8	16	16	US-10-465-826-27	Sequence 7, Appl1
24	70	77.8	16	16	US-10-751-380-7	Sequence 7, Appl1
25	70	77.8	16	16	US-10-688-229-18	Sequence 18, Appl1
26	70	77.8	16	16	US-10-722-176A-6	Sequence 6, Appl1
27	70	77.8	16	16	US-10-722-176A-9	Sequence 7, Appl1
28	70	77.8	16	16	US-10-148-457A-5	Sequence 5, Appl1
29	70	77.8	16	17	US-10-823-259-37	Sequence 37, Appl1
30	70	77.8	16	17	US-10-823-254-37	Sequence 37, Appl1
31	70	77.8	16	17	US-10-916-185-16	Sequence 16, Appl1
32	70	77.8	16	17	US-10-700-971C-7	Sequence 7, Appl1
33	70	77.8	16	18	US-10-927-262A-45	Sequence 45, Appl1
34	70	77.8	16	18	US-10-319-316-5	Sequence 5, Appl1
35	70	77.8	16	18	US-10-878-175B-37	Sequence 37, Appl1
36	70	77.8	16	18	US-10-991-286A-46	Sequence 46, Appl1
37	70	77.8	16	19	US-11-027-967-4	Sequence 4, Appl1
38	70	77.8	16	20	US-11-004-795A-117	Sequence 117, App
39	70	77.8	16	20	US-11-004-379-22	Sequence 22, Appl1
40	70	77.8	16	20	US-11-004-794A-101	Sequence 101, App
41	70	77.8	20	12	US-09-777-560-19	Sequence 19, Appl1
42	70	77.8	20	20	US-11-066-657-1058	Sequence 1058, Ap
43	70	77.8	20	20	US-11-066-657-1060	Sequence 1060, Ap
44	70	77.8	22	14	US-10-136-728-45	Sequence 45, Appl1
45	70	77.8	22	16	US-10-688-299-45	Sequence 45, Appl1

#### ALIGNMENTS

RESULT 1  
US-09-777-560-1  
Sequence 1, Application US/09777560  
Publication No. US20050130884A1  
GENERAL INFORMATION:  
APPLICANT: BRANDT, CURTIS R.  
TITLE OF INVENTION: PHARMACOLOGICALLY ACTIVE ANTIVIRAL PEPTIDES AND METHODS  
TITLE OF INVENTION: OF THEIR USE  
FILE REFERENCE: 032026-0460  
CURRENT APPLICATION NUMBER: US/09/777,560  
CURRENT FILING DATE: 2001-02-06  
PRIOR APPLICATION NUMBER: 60/184,057  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: 60/180,823  
PRIOR FILING DATE: 2000-02-07  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: Patentin Ver. 3.2  
SEQ ID NO 1  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-777-560-1  
Query Match 100.0%; Score 90; DB 12; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.6e-06;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 1 RRKKAVALLPVALLALAP 20  
1 RRKKAVALLPVALLALAP 20

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OM protein - protein search, using sw model

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(Without alignments)  
35.547 Million cell updates/sec

Title: US-09-777-560-1

Perfect score: 90

Sequence: 1 RKKRAVALPVALALAP 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCUTS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfilest.pep:\*

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score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	80	88.9	29	2	US-08-928-958-24
2	80	88.9	29	2	US-09-072-429-24
3	80	88.9	30	2	US-08-928-958-1
4	80	88.9	30	2	US-09-072-429-1
5	80	88.9	30	2	US-09-072-429-1
6	70	77.8	16	1	US-08-642-493-1
7	70	77.8	16	1	US-08-258-852-5
8	70	77.8	16	2	US-08-928-958-4
9	70	77.8	16	2	US-09-072-429-4
10	70	77.8	16	3	US-08-964-302A-3
11	70	77.8	16	3	US-09-170-754B-5
12	70	77.8	16	3	US-09-441-416A-3
13	70	77.8	16	3	US-09-411-706-1
14	70	77.8	16	3	US-09-230-548-19
15	70	77.8	16	4	US-09-450-071A-5
16	70	77.8	16	4	US-09-935-032-1
17	70	77.8	16	4	US-10-083-889-7
18	70	77.8	16	4	US-10-116-288A-23
19	70	77.8	16	4	US-10-144-549-18
20	70	77.8	16	5	PCT-US95-07539-5
21	70	77.8	24	3	US-09-230-548-21
22	70	77.8	25	3	US-08-258-852-1
23	70	77.8	26	1	US-08-258-852-3
24	70	77.8	26	1	US-08-258-852-8
25	70	77.8	26	1	US-08-258-852-9
26	70	77.8	26	2	US-08-928-958-2
27	70	77.8	26	2	US-08-928-958-5

28	70	77.8	26	2	US-09-072-429-2	Sequence 2, Appl1
29	70	77.8	26	2	US-09-072-429-5	Sequence 5, Appl1
30	70	77.8	26	3	US-09-170-754B-1	Sequence 1, Appl1
31	70	77.8	26	3	US-09-170-754B-3	Sequence 1, Appl1
32	70	77.8	26	3	US-09-170-754B-3	Sequence 8, Appl1
33	70	77.8	26	3	US-09-170-754B-9	Sequence 9, Appl1
34	70	77.8	26	4	US-09-450-071A-1	Sequence 1, Appl1
35	70	77.8	26	4	US-09-450-071A-3	Sequence 1, Appl1
36	70	77.8	26	4	US-09-450-071A-8	Sequence 8, Appl1
37	70	77.8	26	4	US-09-450-071A-9	Sequence 8, Appl1
38	70	77.8	26	4	US-09-450-071A-13	Sequence 13, Appl1
39	70	77.8	26	4	US-09-997-465B-1	Sequence 1, Appl1
40	70	77.8	26	5	PCT-US95-07539-1	Sequence 1, Appl1
41	70	77.8	26	5	PCT-US95-07539-3	Sequence 3, Appl1
42	70	77.8	26	5	PCT-US95-07539-8	Sequence 8, Appl1
43	70	77.8	26	5	PCT-US95-07539-9	Sequence 9, Appl1
44	70	77.8	28	1	US-08-258-852-4	Sequence 4, Appl1
45	70	77.8	28	3	US-09-170-754B-4	Sequence 4, Appl1

#### ALIGNMENTS

RESULT 1  
US-08-928-958-24  
Sequence 24, Application US/08928958  
Patent No. 5877282  
GENERAL INFORMATION:  
APPLICANT: NADLER, STEVEN G.  
APPLICANT: CLEVELAND, JEFFREY S.  
APPLICANT: BLAKE, JAMES  
APPLICANT: HAFAR, OMAR K.  
TITLE OF INVENTION: PEPTIDE INHIBITORS OF NUCLEAR PROTEIN  
TITLE OF INVENTION: TRANSLLOCATION HAVING NUCLEAR LOCALIZATION SEQUENCES AND  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSER: ROBINS & ASSOCIATES  
STREET: 90 MIDDLEFIELD ROAD, SUITE 200  
CITY: MENLO PARK  
STATE: CA  
COUNTRY: USA  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/928,958  
FILING DATE: 12-SEP-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/026978  
FILING DATE: 20-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: ROBINS, ROBERTA L.  
REGISTRATION NUMBER: 33,208  
REFERENCE/DOCKET NUMBER: 5998-0019  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 325-7812  
TELEFAX: (650) 325-7823  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 amino acids  
TYPE: amino acid  
STRANDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-928-958-24  
Query Match 88.9%; Score 80; DB 2; Length 29;  
Best Local Similarity 90.0%; Pred. No. 1.2e-05;

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OM protein - protein search, using sw model

Run on: September 12, 2005, 19:29:47 ; Search time 167 Seconds  
(without alignments)  
61.327 Million cell updates/sec

Title: US-09-777-560-1

Perfect score: 90

Sequence: 1 RRRKAAVALPVALIALAP 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Search: 1612378 seqs, 512079187 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Hit No.	Score	Query Match Length	ID	Description
1	70	77.8	206 1	PGF4_HUMAN
2	63	70.0	206 1	PGF4_BOVIN
3	55	61.1	74 2	Q9HRE2
4	53	58.9	100 2	Q92R04
5	51.5	57.2	450 1	ACHX_HUMAN
6	50	55.6	177 2	Q8Y713
7	50	55.6	828 1	CADM_HUMAN
8	49	54.4	177 2	Q720F8
9	49	54.4	194 1	PGF4_CHICK
10	49	54.4	206 2	Q9KZV1
11	49	54.4	346 1	Q6W2C3
12	49	54.4	488 2	MM11_HUMAN
13	49	54.4	488 2	Q6BEZ6
14	48	53.3	167 2	Q53527
15	48	53.3	167 2	Q7VEM9
16	48	53.3	340 2	Q88PY1
17	48	53.3	417 1	MU2A_CLOAB
18	48	53.3	468 2	Q6MS76
19	48	53.3	529 2	Q6CNA8
20	47.5	52.8	447 2	Q91LBS
21	47	52.2	285 2	Q72FG9
22	47	52.2	286 2	Q9NDG2
23	47	52.2	317 2	Q91174
24	47	52.2	328 2	Q848W5
25	47	52.2	407 2	Q89MR3
26	47	52.2	428 2	Q89MR3
27	47	52.2	551 2	Q89MR3
28	46	51.1	202 2	Q9RU46
29	46	51.1	267 2	Q8BIV1
30	46	51.1	353 2	Q8U798
31	46	51.1	353 2	Q8U798

Hit No.	Score	Query Match Length	ID	Description
32	46	51.1	417 1	MU2A_THETA
33	46	51.1	418 1	MU2A_CLOAB
34	46	51.1	431 2	Q9AM70
35	46	51.1	601 2	Q82BE2
36	45	50.0	100 2	Q8UGP5
37	45	50.0	217 2	Q82NL9
38	45	50.0	255 2	Q91LY6
39	45	50.0	289 2	Q8V063
40	45	50.0	289 2	Q65FH4
41	45	50.0	419 1	MU2A_STAM
42	45	50.0	419 1	MU2A_STAM
43	45	50.0	419 1	MU2A_STAM
44	45	50.0	419 1	MU2A_STAM
45	45	50.0	419 2	Q6G7I6

## ALIGNMENTS

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1	70	77.8	206 1	PGF4_HUMAN
2	63	70.0	206 1	PGF4_BOVIN
3	55	61.1	74 2	Q9HRE2
4	53	58.9	100 2	Q92R04
5	51.5	57.2	450 1	ACHX_HUMAN
6	50	55.6	177 2	Q8Y713
7	50	55.6	828 1	CADM_HUMAN
8	49	54.4	177 2	Q720F8
9	49	54.4	194 1	PGF4_CHICK
10	49	54.4	206 2	Q9KZV1
11	49	54.4	346 1	Q6W2C3
12	49	54.4	488 2	MM11_HUMAN
13	49	54.4	488 2	Q6BEZ6
14	48	53.3	167 2	Q53527
15	48	53.3	167 2	Q7VEM9
16	48	53.3	340 2	Q88PY1
17	48	53.3	417 1	MU2A_CLOAB
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45	45	50.0	419 2	Q6G7I6

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43	45	50.0	419 1	MU2A_STAM
44	45	50.0	419 1	MU2A_STAM
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32	46	51.1	417 1	MU2A_THETA
33	46	51.1	418 1	MU2A_CLOAB
34	46	51.1	431 2	Q9AM70
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43	45	50.0	419 1	MU2A_STAM
44	45	50.0	419 1	MU2A_STAM
45	45	50.0	419 2	Q6G7I6

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43	45	50.0	419 1	MU2A_STAM
44	45	50.0	419 1	MU2A_STAM
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39	45	50.0	289 2	Q8V063
40	45	50.0	289 2	Q65FH4
41	45	50.0	419 1	MU2A_STAM
42	45	50.0	419 1	MU2A_STAM
43	45	50.0	419 1	MU2A_STAM
44	45	50.0	419 1	MU2A_STAM
45	45	50.0	419 2	Q6G7I6

Hit No.	Score	Query Match Length	ID	Description
32	46	51.1	417 1	MU2A_THETA
33	46	51.1	418 1	MU2A_CLOAB
34	46	51.1	431 2	Q9AM70
35	46	51.1	601 2	Q82BE2
36	45	50.0	100 2	Q8UGP5
37	45	50.0	217 2	Q82NL9
38	45	50.0	255 2	Q91LY6
39	45	50.0	289 2	Q8V063
40	45	50.0	289 2	Q65FH4
41	45	50.0	419 1	MU2A_STAM
42	45	50.0	419 1	MU2A_STAM
43	45	50.0	419 1	MU2A_STAM
44	45	50.0	419 1	MU2A_STAM
45	45	50.0	419 2	Q6G7I6

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39	45	50.0	289 2	Q8V063
40	45	50.0	289 2	Q65FH4
41	45	50.0	419 1	MU2A_STAM
42	45	50.0	419 1	MU2A_STAM
43	45	50.0	419 1	MU2A_STAM
44	45	50.0	419 1	MU2A_STAM
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37	45	50.0	217 2	Q82NL9
38	45	50.0	255 2	Q91LY6
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40	45	50.0	289 2	Q65FH4
41	45	50.0	419 1	MU2A_STAM
42	45	50.0	419 1	MU2A_STAM
43	45	50.0	419 1	MU2A_STAM
44	45	50.0	419 1	MU2A_STAM
45	45	50.0	419 2	Q6G7I6

ID	PGFA_HUMAN	STANDARD;	PRT;	206 AA.
AC	P08620;			
AD	01-AUG-1988 (Rel. 08, Created)			
DT	01-AUG-1988 (Rel. 08, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Fibroblast growth factor-4 precursor (FGF-4) (Heparin secretory transforming protein) (HST-1) (HST) (Transforming protein KS3) (HBGF-4).			
DE	Name=FGF4; Synonyms=HST, HSTF1, KS3;			
GN	Homo sapiens (Human).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RA	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=86041096; PubMed=2959959;			
RA	Yoshida T., Miyagawa K., Odagiri H., Sakamoto H., Little P.F.R., Terada M., Sugimura T.;			
RT	"Genomic sequence of hst, a transforming gene encoding a protein homologous to fibroblast growth factors and the int-2-encoded protein.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 84:7305-7309(1987).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87204251; PubMed=2953031;			
RA	Taira M., Yoshida T., Miyagawa K., Sakamoto H., Terada M., Sugimura T.;			
RT	"cDNA sequence of human transforming gene hst and identification of the coding sequence required for transforming activity.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 84:2980-2984(1987).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87301716; PubMed=2957062; DOI=10.1016/0092-8674(87)90331-X;			
RA	Deilli Bovy F., Curatola A.M., Kern F.G., Greco A., Ittmann M., Basiglio C.;			
RT	"An oncogene isolated by transfection of Kaposi's sarcoma DNA encodes a growth factor that is a member of the FGF family.";			
RL	Cell 50:729-737(1987).			
RN	[4]			
RP	X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 79-206.			
RX	PubMed=14486033; DOI=10.1126/MCB.21.17.5946-5957.2001;			
RA	Bellosta P., Iwahori A., Plotnikov A.N., Bilsenkova A.V., Basiglio C., Mohammadi M.;			
RT	"Identification of receptor and heparin binding sites in fibroblast growth factor 4 by structure-based mutagenesis.";			
RL	Mol. Cell. Biol. 21:5946-5957(2001).			
CC	-1- FUNCTION: Can transform NIH 3T3 cells from a human stomach tumor (hst) and from kaposi's sarcoma (KS3). It has a mitogenic activity.			
CC	-1- SIMILARITY: Belongs to the heparin-binding growth factors family.			
CC	This SWISS-PROT entry is copyright It is produced through a collaboration			

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OM protein - protein search, using sw model

Run on: September 12, 2005, 19:38:07; Search time 39 seconds  
(without alignments)  
49.342 Million cell updates/sec

Title: US-09-777-560-1

Perfect score: 90

Sequence: 1 RRKRAVALPALVALALAP 20

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	70	77.8	206	1	TYVHUS
2	63	70.0	206	2	UC4268
3	55	61.1	74	2	D84231
4	50	55.6	177	2	AH1232
5	49	54.4	194	2	I50710
6	49	54.4	488	2	S13423
7	48	53.3	167	2	A70862
8	47	52.2	317	2	B83344
9	46	51.1	202	2	D75383
10	46	51.1	353	2	AH1116
11	46	51.1	353	2	E98170
12	46	51.1	418	2	B97334
13	46	51.1	1251	2	A57293
14	45	50.0	100	2	A82710
15	45	50.0	100	2	A82710
16	45	50.0	419	2	A99906
17	45	50.0	423	2	AH1393
18	45	50.0	423	2	AC1769
19	45	50.0	428	2	H84122
20	45	50.0	429	2	G33554
21	45	50.0	441	2	S41710
22	45	50.0	556	2	T46842
23	45	50.0	557	2	H97351
24	45	50.0	858	2	T08881
25	44	48.9	244	2	S36245
26	44	48.9	244	2	UC8019
27	44	48.9	419	2	A95125
28	44	48.9	419	2	B97995
29	44	48.9	512	2	B83060

30	44	48.9	534	2	P90031
31	44	48.9	917	2	B81309
32	44	48.9	1094	2	P70697
33	44	48.9	5376	2	T42215
34	43	47.8	120	2	T44554
35	43	47.8	223	2	B86200
36	43	47.8	334	2	G84123
37	43	47.8	494	2	AC0133
38	43	47.8	660	2	B85499
39	43	47.8	660	2	B90648
40	43	47.8	660	2	A64739
41	43	47.8	1230	2	S47466
42	42.5	47.2	1308	2	T15280
43	42	46.7	219	2	A80945
44	42	46.7	253	2	G71560
45	42	46.7	256	2	T35133

## ALIGNMENTS

RESULT 1  
TYVHUS  
fibroblast growth factor 4 - human  
N.Alternate names: heparin secretory transforming protein 1; Kaposi sarcoma oncogene;  
C.Species: Homo sapiens (man)  
C.Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 09-Jul-2004  
C.Accession: A28417; A29876; A29649  
R.Yoshida, T.; Miyagawa, K.; Odagiri, H.; Sakamoto, H.; Little, P.F.R.; Terada, M.; Su  
Proc. Natl. Acad. Sci. U.S.A. 84, 7305-7309, 1987  
A.Title: Genomic sequence of het, a transforming gene encoding a protein homologous to  
A.Reference number: A28417; MUID:86041096; PMID:2959595  
A.Accession: A28417  
A.Molecule type: DNA  
A.Residues: 1-206 <YOS>  
A.Cross-references: UNIPROT:P08620; DDBJ:J02986; NID:G184430; PIDN:AAB59555.1; PID:G38  
R.Taira, M.; Yoshida, T.; Miyagawa, K.; Sakamoto, H.; Terada, M.; Sugimura, T.  
Proc. Natl. Acad. Sci. U.S.A. 84, 2980-2984, 1987  
A.Title: cDNA sequence of human transforming gene het and identification of the coding  
A.Reference number: A29876; MUID:87204251; PMID:2953031  
A.Accession: A29876  
A.Molecule type: mRNA  
A.Residues: 1-206 <TAI>  
A.Cross-references: GB:J02986; GB:M16338; NID:G184430; PIDN:AAB59555.1; PID:G386788  
R.Delll Boyl, P.; Curatola, A.M.; Kern, F.G.; Greco, A.; Ittmann, M.; Basilico, C.  
Cell 50, 729-737, 1987  
A.Title: An oncogene isolated by transfection of Kaposi's sarcoma DNA encodes a growth  
A.Reference number: A29649; MUID:87301716; PMID:2957062  
A.Accession: A29649  
A.Molecule type: mRNA  
A.Residues: 1-206 <BOV>  
A.Cross-references: GB:M17446; NID:G186785; PIDN:AAB59473.1; PID:G307092  
C.Comment: This protein is an oncogene for Kaposi's sarcoma. It is homologous to the m  
C.Genetic: GDB:FCF4; HSTF1  
A.Gene: GDB:FCF4; HSTF1  
A.Cross-references: GDB:120066; OMIM:164980  
A.Map position: 11q13.3-11q13.3  
A.Introns: 114/1; 148/3  
C.Superfamily: fibroblast growth factor  
C.Keywords: growth factor; Kaposi sarcoma; transforming protein

Query Match 77.8%; Score 70; DB 1; Length 206;  
Best Local Similarity 100.0%; Pred. No. 0.0038;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Or 5 AAVALPALVALALAP 20  
Db 7 AAVALPALVALALAP 22

RESULT 2  
JC4268  
fibroblast growth factor 4 - bovine

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 12, 2005, 19:29:07 : Search time 164 Seconds

(without alignments)  
47.166 Million cell updates/sec

Title: US-09-777-560-1  
Perfect score: 90  
Sequence: 1 RRKKAVALLPVLLALAP 20

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16dec04:\*  
1: geneeqp19808:\*  
2: geneeqp19908:\*  
3: geneeqp20008:\*  
4: geneeqp20018:\*  
5: geneeqp20028:\*  
6: geneeqp20038:\*  
7: geneeqp20048:\*  
8: geneeqp20058:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	90	100.0	20	AAE12478	Aae12478 Membrane
2	90	100.0	20	AAE12477	Aae12477 Membrane
3	84	93.3	20	AAE12476	Aae12476 Membrane
4	84	93.3	20	AAE12475	Aae12475 Membrane
5	82	91.1	19	AAE12474	Aae12474 Membrane
6	82	91.1	22	AAE12473	Aae12473 Membrane
7	80	88.9	29	AAE12472	Aae12472 Membrane
8	80	88.9	29	AAE12471	Aae12471 Membrane
9	80	88.9	29	AAE12470	Aae12470 Membrane
10	80	88.9	30	AAE12469	Aae12469 Membrane
11	75	83.3	17	AAE12468	Aae12468 Membrane
12	75	83.3	17	AAE12467	Aae12467 Membrane
13	75	83.3	20	AAE12466	Aae12466 Membrane
14	75	83.3	27	AAE12465	Aae12465 Membrane
15	75	83.3	27	AAE12464	Aae12464 Membrane
16	73	81.1	29	AAE12463	Aae12463 Membrane
17	72.5	80.6	20	AAE12462	Aae12462 Membrane
18	70	77.8	16	AAE12461	Aae12461 Membrane
19	70	77.8	16	AAE12460	Aae12460 Membrane
20	70	77.8	16	AAE12459	Aae12459 Membrane
21	70	77.8	16	AAE12458	Aae12458 Membrane
22	70	77.8	16	AAE12457	Aae12457 Membrane
23	70	77.8	16	AAE12456	Aae12456 Membrane
24	70	77.8	16	AAE12455	Aae12455 Membrane
25	70	77.8	16	AAE12454	Aae12454 Membrane

26	70	77.8	16	AAE12479	Aae12479 Membrane
27	70	77.8	16	AAE12478	Aae12478 Membrane
28	70	77.8	16	AAE12477	Aae12477 Membrane
29	70	77.8	16	AAE12476	Aae12476 Membrane
30	70	77.8	16	AAE12475	Aae12475 Membrane
31	70	77.8	16	AAE12474	Aae12474 Membrane
32	70	77.8	16	AAE12473	Aae12473 Membrane
33	70	77.8	16	AAE12472	Aae12472 Membrane
34	70	77.8	16	AAE12471	Aae12471 Membrane
35	70	77.8	16	AAE12470	Aae12470 Membrane
36	70	77.8	16	AAE12469	Aae12469 Membrane
37	70	77.8	16	AAE12468	Aae12468 Membrane
38	70	77.8	16	AAE12467	Aae12467 Membrane
39	70	77.8	16	AAE12466	Aae12466 Membrane
40	70	77.8	16	AAE12465	Aae12465 Membrane
41	70	77.8	16	AAE12464	Aae12464 Membrane
42	70	77.8	16	AAE12463	Aae12463 Membrane
43	70	77.8	16	AAE12462	Aae12462 Membrane
44	70	77.8	16	AAE12461	Aae12461 Membrane
45	70	77.8	16	AAE12460	Aae12460 Membrane

## ALIGNMENTS

RESULT 1  
ID AAE12478 standard, peptide; 20 AA.

XX AAE12478;  
XX 03-JAN-2002 (first entry)

XX Membrane transiting antiviral peptide bbb.

XX Membrane transiting peptide; virucide; antiviral; Herpes Simplex Virus;  
XX HSV; HIV; Human Immunodeficiency Virus; CMV; Cytomegalovirus.

XX Unidentified.

XX Key Location/Qualifiers

XX Modified-site 1 /note= "Biotin-aminohexanoyl Arg"

XX WO200157072-A2.

XX 09-AUG-2001.

XX 06-FEB-2001; 2001WO-US003813.

XX 07-FEB-2000; 2000US-0180823P.

XX 22-FEB-2000; 2000US-0184057P.

XX (WISC) WISCONSIN ALUMNI RES FOUND.

XX Brandt C, Bullmann H;

XX WPI; 2001-638840/73.

XX Peptides comprising membrane transiting peptides useful for treating or preventing a virus infection, e.g., human immunodeficiency virus, herpes simplex virus and cytomegalovirus.

XX Claim 7; Page 15; 43pp; English.

XX The invention relates to peptides comprising membrane transiting peptides with antiviral properties. The peptides are useful for treating or preventing a virus infection in a warm blooded animal, e.g., enveloped viruses such as human immunodeficiency virus (HIV), herpes simplex virus (HSV), cytomegalovirus (CMV) and non-enveloped virus. Preferably, the peptides are useful for treating or preventing infections from one or more HSVs. The antiviral peptides are used for treating viral infections of the skin or part of the oral or genital cavity. The present sequence